WHAT IS CLAIMED IS:

1. A plant promoter comprising at least one synthetic multimeric promoter element region having a nucleotide sequence selected from the group consisting of:

a) a nucleotide sequence comprising six DRE 1 (SEQ ID NO.: 59), two ABRE1 (SEQ ID NO.: 2), three As-1 (SEQ ID NO.: 7), one GT-2 (SEQ ID NO.: 24), and two PCNA IIA (SEQ ID NO.: 45) promoter elements;

b) a nucleotide sequence comprising three DRE 1 (SEQ ID NO.: 59), three ABRE1 (SEQ ID NO.: 2), one As-1 (SEQ ID NO.: 7), two GT-2 (SEQ ID NO.: 24), and two PCNA IIA (SEQ ID NO.: 45) promoter elements;

c) a nucleotide sequence comprising five DRE 1 (SEQ ID NO.: 59), three ABRE1 (SEQ ID NO.: 2), two As-1 (SEQ ID NO.: 7), and five GT-2 (SEQ ID NO.: 24) promoter elements;

d) a nucleotide sequence comprising four DRE 1 (SEQ ID NO.: 59), three ABRE1 (SEQ ID NO.: 2), three GT-2 (SEQ ID NO.: 24), and one PCNA IIA (SEQ ID NO.: 45) promoter elements;

e) a nucleotide sequence comprising two DRE 1 (SEQ ID NO.: 59), one ABRE1 (SEQ ID NO.: 2), five As-1 (SEQ ID NO.: 7), one GT-2 (SEQ ID NO.: 24), and three PCNA IIA (SEQ ID NO.: 45) promoter elements;

f) a nucleotide sequence comprising five DRE 1 (SEQ ID NO.: 59), two ABRE1 (SEQ ID NO.: 2), one As-1 (SEQ ID NO.: 7), one GT-2 (SEQ ID NO.: 24), and two PCNA IIA (SEQ ID NO.: 45) promoter elements;

g) a nucleotide sequence comprising one DRE 1 (SEQ ID NO.: 59), two ABRE1 (SEQ ID NO.: 2), two As-1 (SEQ ID NO.: 7), and one GT-2 (SEQ ID NO.: 24) promoter elements;

h) a nucleotide sequence comprising two DRE 1, one ABRE1 (SEQ ID NO.: 2), three As-1 (SEQ ID NO.: 7), and one GT-2 (SEQ ID NO.: 24) promoter elements; and

i) a nucleotide sequence that hybridizes under stringent conditions to any of the nucleotide sequences of a), b), c), d), e), f), g), and h).

2. The plant promoter of Claim 1 comprising at least one synthetic multimeric promoter element region having a nucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence comprising promoter elements DRE1, ABRE1, DRE1, As-1, ABRE1, DRE1, GT-2, As-1, DRE1, PCNA IIA, PCNA IIA, DRE1, As-1, and DRE1 sequentially (SEQ ID NO.: 66);

(b) a nucleotide sequence comprising promoter elements DRE1, DRE1, As-1, PCNA IIA, ABRE1, PCNA IIA, ABRE1, DRE1, GT-2, GT-2, and ABRE1 sequentially (SEQ ID NO.: 67);

(c) a nucleotide sequence comprising promoter elements GT-2, ABRE1, ABRE1, GT-2, As-1, GT-2, GT-2, DRE1, GT-2, DRE1, DRE1, As-1, DRE1, DRE1, and ABRE1 sequentially (SEQ ID NO.: 65);

(d) a nucleotide sequence comprising promoter elements ABRE1, ABRE1, GT-2, GT-2, GT-2, DRE1, DRE1, DRE1, DRE1, ABRE1 , and PCNA IIA sequentially (SEQ ID NO.: 68);

(e) a nucleotide sequence comprising promoter elements PCNA IIA, As-1, GT-2, As-1, DRE1, As-1, As-1, PCNA IIA, As-1, PCNA IIA, DRE1, and ABRE1 sequentially (SEQ ID NO.: 69);

(f) a nucleotide sequence comprising promoter elements As-1, GT-2, DRE1, DRE1, ABRE1, PCNA IIA, DRE1, PCNA IIA, ABRE1, DRE1, and DRE1 sequentially (SEQ ID NO.: 71);

(g) a nucleotide sequence comprising promoter elements As-1, ABRE1, GT-2, As-1, ABRE1, and DRE1 sequentially (SEQ ID NO.: 72);

(h) a nucleotide sequence comprising promoter elements DRE1, ABRE1, GT-2, DRE1, As-1, As-1, and As-1 sequentially (SEQ ID NO.: 70);

(i) a nucleotide sequence set forth in Figure 7, 8, 9, 10, 11, 12, 13, or 14 (SEQ ID NOS.: 65-72);

(j) a nucleotide sequence that comprises a variant of a nucleotide sequence set forth in Figure 7, 8, 9, 10, 11, 12, 13, or 14 (SEQ ID NOS.: 65-72); and

(k) a nucleotide sequence that hybridizes under stringent conditions to a nucleotide sequence of (a), (b), (c), (d), (e), (f), (g), (h), (i), or (j).

3. A chimeric gene comprising the promoter of claim 2 operably linked to a coding sequence.

4. An expression cassette comprising the chimeric gene of claim 3.

5. A transformation vector comprising the expression cassette of claim 4.

6. A plant stably transformed with the transformation vector of claim 5.

7. A plant, or its parts, having stably incorporated into its genome a DNA construct comprising a plant promoter operably linked to a coding sequence, said plant promoter comprising at least one synthetic multimeric promoter element region (SMPER) that enhances expression of said coding sequence.

8. A plant, or its parts, having stably incorporated into its genome a DNA construct comprising a plant promoter operably linked to a coding sequences, said plant promoter comprising at least one synthetic multimeric promoter element region having a nucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence comprising promoter elements DRE1, ABRE1, DRE1, As-1, ABRE1, DRE1, GT-2, As-1, DRE1, PCNA IIA, PCNA IIA, DRE1, As-1, and DRE1 sequentially (SEQ ID NO.: 66);

(b) a nucleotide sequence comprising promoter elements DRE1, DRE1, As-1, PCNA IIA, ABRE1, PCNA IIA, ABRE1, DRE1, GT-2, GT-2, and ABRE1 sequentially (SEQ ID NO.: 67);

(c) a nucleotide sequence comprising promoter elements GT-2, ABRE1, ABRE1, GT-2, As-1, GT-2, GT-2, DRE1, GT-2, DRE1, DRE1, As-1, DRE1, DRE1, and ABRE1 sequentially (SEQ ID NO.: 65);

(d) a nucleotide sequence comprising promoter elements ABRE1, ABRE1, GT-2, GT-2, GT-2, DRE1, DRE1, DRE1, DRE1, ABRE1, and PCNA IIA sequentially (SEQ ID NO.: 68);

(e) a nucleotide sequence comprising promoter elements PCNA IIA, As-1, GT-2, As-1, DRE1, As-1, As-1, PCNA IIA, As-1, PCNA IIA, DRE1, and ABRE1 sequentially (SEQ ID NO.: 69);

(f) a nucleotide sequence comprising promoter elements As-1, GT-2, DRE1, DRE1, ABRE1, PCNA IIA, DRE1, PCNA IIA, ABRE1, DRE1, and DRE1 sequentially (SEQ ID NO.: 71);

(g) a nucleotide sequence comprising promoter elements As-1, ABRE1, GT-2, As-1, ABRE1, and DRE1 sequentially (SEQ ID NO.: 72);

(h) a nucleotide sequence comprising promoter elements DRE1, ABRE1, GT-2, DRE1, As-1, As-1, and As-1 sequentially (SEQ ID NO.: 70);

(i) a nucleotide sequence set forth in Figure 7, 8, 9, 10, 11, 12, 13, or 14 (SEQ ID NOS.: 65-72);

(j) a nucleotide sequence that comprises a variant of a nucleotide sequence set forth in Figures 7, 8, 9, 10, 11, 12, 13, or 14 (SEQ ID NOS.: 65-72); and

(k) a nucleotide sequence that hybridizes under stringent conditions to a nucleotide sequence of (a), (b), (c), (d), (e), (f), (g), (h), (i), or (j).

9. The plant of claim 8, wherein said plant is a dicot.

10. The plant of claim 8, wherein said plant is a monocot.

11. The plant of claim 10, wherein said monocot is maize.

12. A plant cell having stably incorporated into its genome a DNA construct comprising a plant promoter operably linked to a coding sequence, said plant promoter comprising at least one synthetic multimeric promoter element region having a nucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence comprising promoter elements DRE1, ABRE1, DRE1, As-1, ABRE1, DRE1, GT-2, As-1, DRE1, PCNA IIA, PCNA IIA, DRE1, As-1, and DRE1 sequentially (SEQ ID NO.: 66);

(b) a nucleotide sequence comprising promoter elements DRE1, DRE1, As-1, PCNA IIA, ABRE1, PCNA IIA, ABRE1, DRE1, GT-2, GT-2, and ABRE1 sequentially (SEQ ID NO.: 67);

(c) a nucleotide sequence comprising promoter elements GT-2, ABRE1, ABRE1, GT-2, As-1, GT-2, GT-2, DRE1, GT-2, DRE1, DRE1, As-1, DRE1, DRE1, and ABRE1 sequentially (SEQ ID NO.: 65);

(d) a nucleotide sequence comprising promoter elements ABRE1, ABRE1, GT-2, GT-2, GT-2, DRE1, DRE1, DRE1, DRE1, ABRE1 and PCNA IIA sequentially (SEQ ID NO.: 68);

(e) a nucleotide sequence comprising promoter elements PCNA IIA, As-1, GT-2, As-1, DRE1, As-1, As-1, PCNA IIA, As-1, PCNA IIA, DRE1, and ABRE1 sequentially (SEQ ID NO.: 69);

(f) a nucleotide sequence comprising promoter elements As-1, GT-2, DRE1, DRE1, ABRE1, PCNA IIA, DRE1, PCNA IIA, ABRE1, DRE1, and DRE1 sequentially (SEQ ID NO.: 71);

(g) a nucleotide sequence comprising promoter elements As-1, ABRE1, GT-2, As-1, ABRE1, and DRE1 sequentially (SEQ ID NO.: 72);

(h) a nucleotide sequence comprising promoter elements DRE1, ABRE1, GT-2, DRE1, As-1, As-1, and As-1 sequentially (SEQ ID NO.: 70);

(i) a nucleotide sequence set forth in Figure 7, 8, 9, 10, 11, 12, 13, or 14 (SEQ ID NOS.: 65-72);

(j) a nucleotide sequence that comprises a variant of a nucleotide sequence set forth in Figure 7, 8, 9, 10, 11, 12, 13, or 14 (SEQ ID NOS.: 65-72); and

(k) a nucleotide sequence that hybridizes under stringent conditions to the nucleotide sequence of (a), (b), (c), (d), (e), (f), (g), (h), (i), or (j).

13. The plant cell of claim 12, wherein said plant cell is from a dicotyledonous plant.

14. The plant cell of claim 12, wherein said plant cell is from a monocotyledonous plant.

15. The plant cell of claim 14, wherein said monocotyledonous plant is a maize plant.

16. A method for constitutively expressing a heterologous nucleotide sequence in a plant, said method comprising:

i) transforming a plant cell with a transformation vector comprising an expression cassette, said expression cassette comprising a plant promoter operably linked

to a coding sequence, said plant promoter comprising a synthetic multimeric promoter element region selected from the group consisting of (a), (b), (c), (d), (e), (f), (g), (h), (i), (j), and (k) of claim 1; and

ii) regenerating a stably transformed plant from said transformed cell, said plant having stably incorporated into its genome said expression cassette.

17. A method of selecting promoter elements active in a tissue of interest, comprising

a) isolating or synthesizing oligonucleotides representing known or putative promoter elements or transcription factor binding sites;

b) labeling said oligonucleotides;

c) pooling said oligonucleotides to create an array which facilitates screening;

d) hybridizing said oligonucleotides with nuclear extracts of said tissue of interest; and

e) selecting those oligonucleotides exhibiting preferential binding to said nuclear extracts.

18. A method of creating synthetic multimeric promoter element regions active in a tissue of interest, comprising

a) selecting known or putative promoter elements or transcription factor binding sites which exhibit preferential binding to nuclear extract prepared from said tissue of interest;

b) combining said selected oligonucletides in novel arrangements encompassing variation in number of copies, sequential order, orientation, and spacer regions; and

c) testing said novel arrangements for their effect on transcription and selecting those demonstrating enhancement or suppression of linked gene expression.